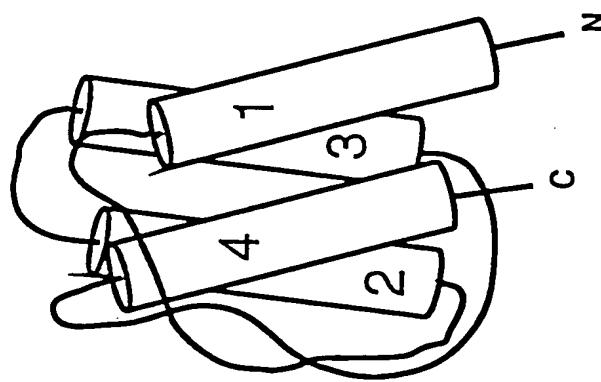


A' G T C T T " H S E P I E G D O

Native Protein



Sequence Rearranged Protein

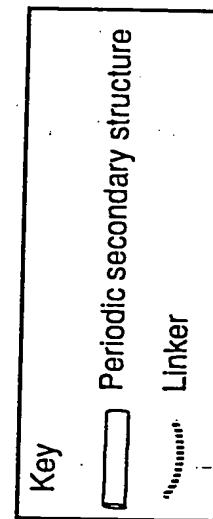
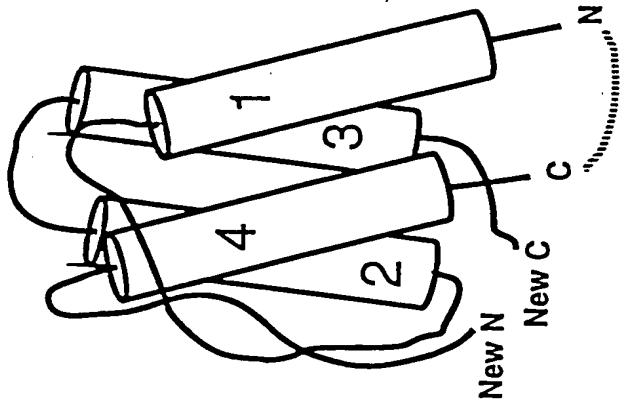
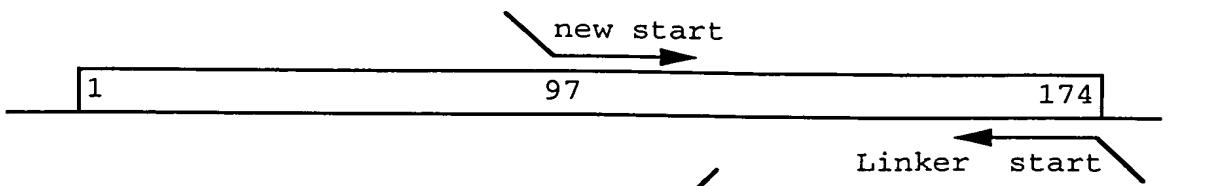
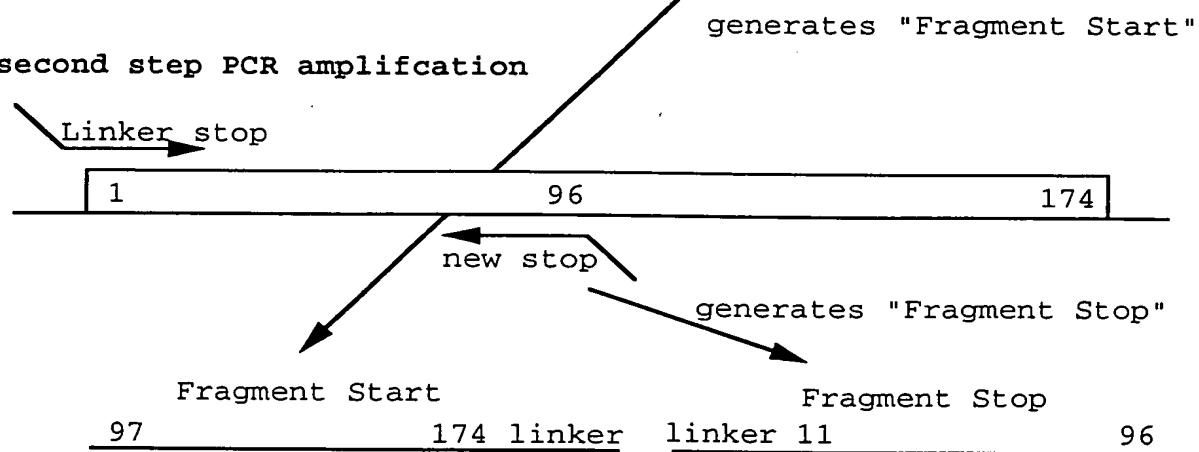


Figure 1

first step PCR amplification



second step PCR amplification



third step PCR amplification

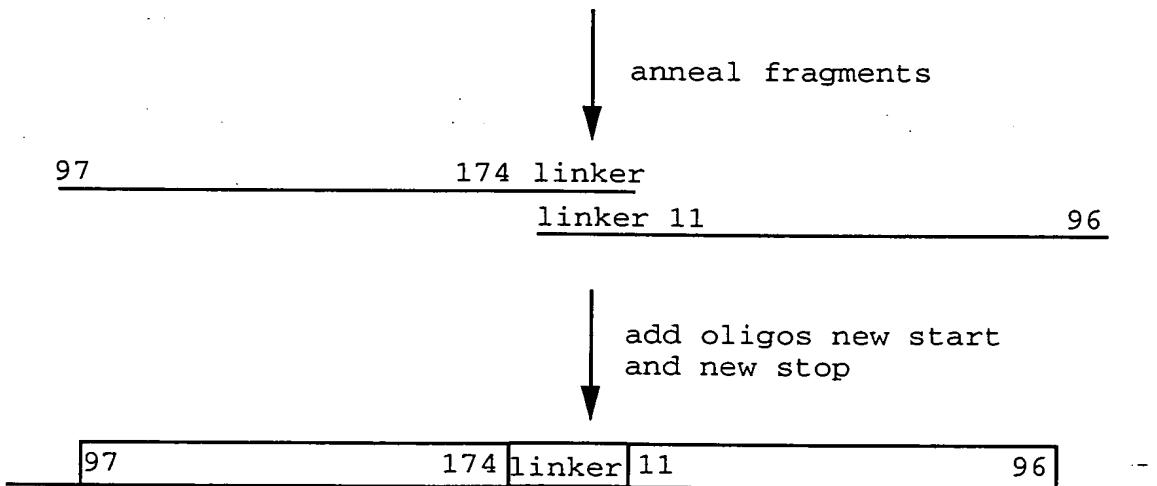
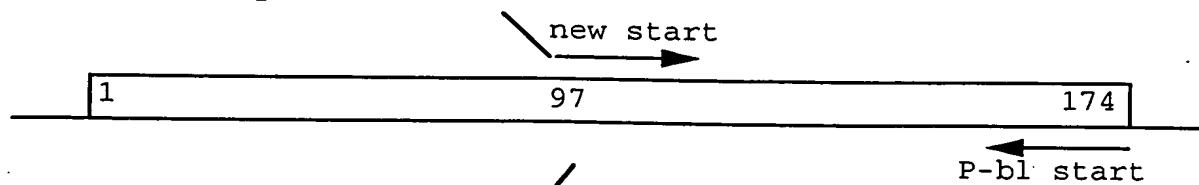
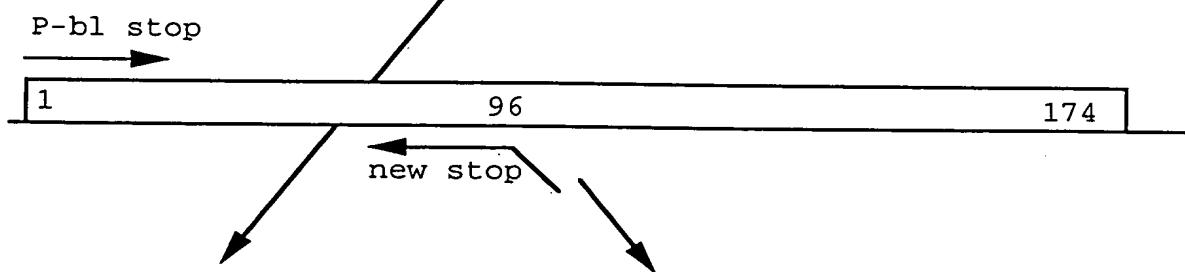


Figure 2.

first step PCR amplification



second step PCR amplification



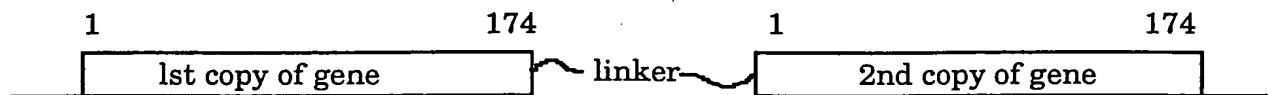
97 174 1 96

↓
ligate fragments

97 174 ; 1 96

Figure 3.

I. Construct tandemly-duplicated template



II. PCR-amplify tandemly-duplicated template

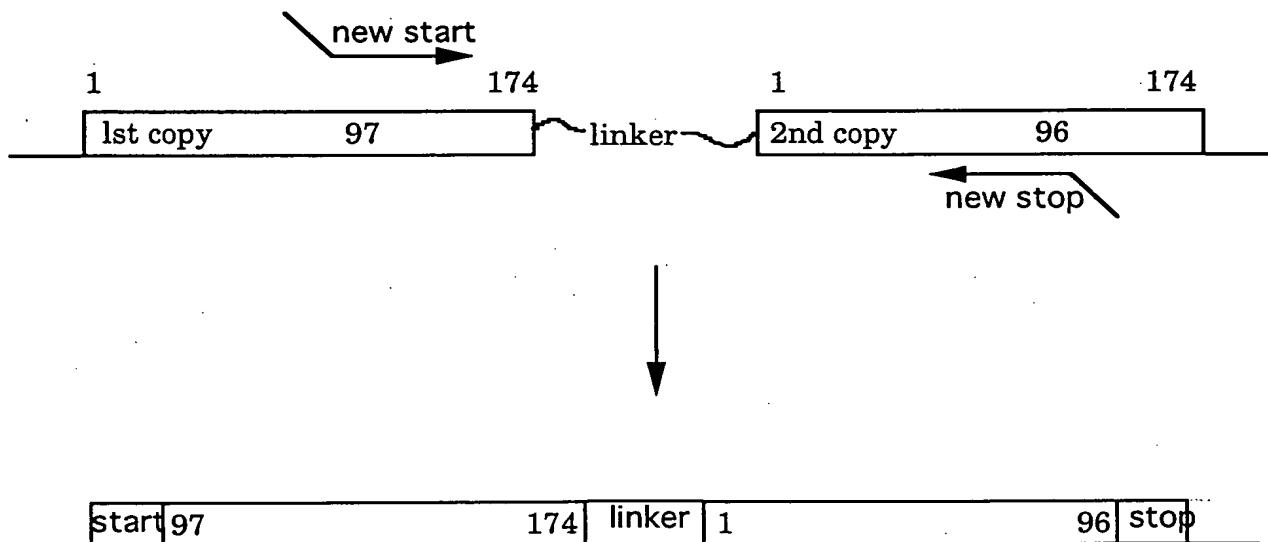


Figure 4.

1 GCCCCACCACGCCCTCATCTGTGACAGCCGAGTCCTGGAGAGGTACCTCTGGAGGCCAAG
 1-----+-----+-----+-----+-----+-----+ 60
 CCGGGTGGTGGAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTT
 AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys
 61 GAGGCCGAGAAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACT
 61-----+-----+-----+-----+-----+-----+ 120
 CTCCGGCTCTTATAGTGTGCCCCGACACGACTTGTGACGTCGAACACTACTCTTATAGTGA
 GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr
 121 GTCCCAGACACCAAAGTTAATTCTATGCCCTGGAAGAGGATGGAGGTGGGGCAGCAGGCC
 121-----+-----+-----+-----+-----+-----+ 180
 CAGGGTCTGGTTTCAATTAAAGATA CGGACCTCTCCTACCTCCAGCCGTCGTCCGG
 ValProAspThrLysValAsnPheTyrAlaTrpLysArgMetGluValGlyGlnGlnAla
 181 GTAGAAAGTCTGGCAGGGCCTGGCCCTGCTGCGAACGCTGTCCTGCGGGGCCAGGCCCTG
 181-----+-----+-----+-----+-----+-----+ 240
 CATCTTCAGACCGTCCCGGACCGGGACGACAGCCTTGACAGGACGCCCGGTCCGGAC
 ValGluValTrpGlnGlyLeuAlaLeuSerGluAlaValLeuArgGlyGlnAlaLeu
 241 TTGGTCAACTCTTCCCAGCCGTGGAGCCCTGCAGCTGCATGTGGATAAAGCCGTCACT
 241-----+-----+-----+-----+-----+-----+ 300
 AACCAAGTTGAGAAGGGTGGCACCCCTGGGACGTCGACGTACACCTATTCGGCAGTCA
 LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer
 301 GCCCTTCGCAGCCTCACCACTCTGCTTGGCTCTGGAGGCCAGAAGGAAGCCATCTCC
 301-----+-----+-----+-----+-----+-----+ 360
 CCGGAAGCGTCGGAGTGGTGAGAAGAACCGAGACCCCTGGGTCTTCCTTCGGTAGAGG
 GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer
 361 CCTCCAGATGCCCTCAGCTGCTCCACTCCGAACAATCAGCTGACACTTCGGAAA
 361-----+-----+-----+-----+-----+-----+ 420
 GGAGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTAGTGACCACTGTGAAAGGCCTT
 ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys
 421 CTCTTCCGAGTCTACTCCAATTTCCTCCGGGAAAGCTGAAGCTGTACACAGGGAGGCC
 421-----+-----+-----+-----+-----+-----+ 480
 GAGAAGGCTCAGATGAGGTTAAAGGAGGCCCTTCGACTTCGACATGTGCCCCCTCCGG
 LeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla
 481 TGCAAGGACAGGGACAGATGA
 481-----+-----+-----+-----+-----+-----+ 501
 ACGTCCTGTCCCCCTGTCTACT
 CysArgThrGlyAspArg

Figure 5